STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/590, 457_

Source: _PCT_

Date Processed by STIC: _09/05/2006_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/590,457_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length
The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII
The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or **Xaa**, and which residue n or **Xaa** represents.

10.____Invalid <213>
Response
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11____Use of <220>
Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12____PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa
"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

PCT

```
   3 <110> APPLICANT: Cirpus, Petra
   4         Bauer, Jorg
   5         Qiu, Xiao
   6         Wu, Guohai
   7         Datla, Nagamani
   9 <120> TITLE OF INVENTION: METHOD FOR PRODUCING POLYUNSATURATED FATTY ACIDS IN
TRANSGENIC
  10         PLANTS
  12 <130> FILE REFERENCE: 13987-00020-US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/590,457
C--> 14 <141> CURRENT FILING DATE: 2006-08-25
  14 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/001863
  15 <151> PRIOR FILING DATE: 2005-02-23
  17 <150> PRIOR APPLICATION NUMBER: DE 10 2004 009 457.8
  18 <151> PRIOR FILING DATE: 2004-02-27
  20 <150> PRIOR APPLICATION NUMBER: DE 10 2004 012 370.5
  21 <151> PRIOR FILING DATE: 2004-03-13
  23 <150> PRIOR APPLICATION NUMBER: DE 10 2004 017 518.7
  24 <151> PRIOR FILING DATE: 2004-04-08
  26 <150> PRIOR APPLICATION NUMBER: DE 10 2004 024 014.0
  27 <151> PRIOR FILING DATE: 2004-05-14
  29 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/07957
  30 <151> PRIOR FILING DATE: 2004-07-16
  32 <150> PRIOR APPLICATION NUMBER: DE 10 2004 062 543.3
  33 <151> PRIOR FILING DATE: 2004-12-24
  35 <160> NUMBER OF SEQ ID NOS: 255
  37 <170> SOFTWARE: PatentIn version 3.3
  40 <210> SEQ ID NO: 1
  41 <211> LENGTH: 1266
  42 <212> TYPE: DNA
  43 <213> ORGANISM: Euglena gracilis
  45 <220> FEATURE:
  46 <221> NAME/KEY: CDS
  47 <222> LOCATION: (1)..(1266)
  48 <223> OTHER INFORMATION: Delta-8 desaturase
  50 <400> SEQUENCE: 1
  51 atg aag tca aag cgc caa gcg ctt ccc ctt aca att gat gga aca aca      48
  52 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
  53 1               5                   10                  15
  56 tat gat gtg tct gcc tgg gtc aat ttc cac cct ggt ggt gcg gaa att      96
  57 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
  58              20                  25                  30
  60 ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg     144
  61 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
```

Cpg-7)
Does Not Comply
Corrected Diskette Needed

Cps-6)

```
62        35                40                45
64 cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat    192
65 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
66    50                55                60
68 ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag    240
69 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
70 65                70                75                80
72 gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat    288
73 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
74                85                90                95
76 gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt    336
77 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
78                100                105                110
80 gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att    384
81 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
82        115                120                125
84 ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct    432
85 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
86    130                135                140
89 cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac    480
90 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
91 145                150                155                160
93 ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca    528
94 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
95                165                170                175
97 tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa    576
98 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
99                180                185                190
101 ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag    624
102 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
103                195                200                205
105 gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc    672
106 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
107        210                215                220
109 cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg    720
110 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
111 225                230                235                240
113 tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac    768
114 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
115                245                250                255
117 caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg    816
118 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
119                260                265                270
122 cat tgg aca ttg aag gcc ctg ttc cac tta ttc ttt atg ccc agc atc    864
123 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
124        275                280                285
126 ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc    912
127 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
128        290                295                300
```

RAW SEQUENCE LISTING   DATE: 09/05/2006
PATENT APPLICATION: US/10/590,457   TIME: 15:11:48

Input Set : **E:\Sequence Listing-13987-00020-US.txt**
Output Set: **N:\CRF4\09052006\J590457.raw**

```
130 ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc      960
131 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
132 305                     310             315                 320
134 ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat     1008
135 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
136                         325             330                 335
138 gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga     1056
139 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
140                         340             345                 350
142 ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc     1104
143 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
144             355                 360             365
146 cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag     1152
147 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
148     370                 375                 380
150 cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc     1200
151 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
152 385             390                 395                 400
155 ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc     1248
156 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
157                 405                 410             415
159 gcg ggg aag gct cta taa                                             1266
160 Ala Gly Lys Ala Leu
161                 420
164 <210> SEQ ID NO: 2
166 <211> LENGTH: 421
168 <212> TYPE: PRT
170 <213> ORGANISM: Euglena gracilis
174 <400> SEQUENCE: 2
176 Met Lys Ser Lys Arg Gln Ala Leu Pro Leu Thr Ile Asp Gly Thr Thr
177 1                   5                   10                  15
180 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
181             20                  25                  30
184 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
185         35                  40                  45
188 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
189     50                  55                  60
192 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
193 65                  70                  75                  80
196 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
197             85                  90                  95
200 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
201             100                 105                 110
204 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
205         115                 120                 125
208 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
209     130                 135                 140
212 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
213 145                 150                 155                 160
```

```
216 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
217             165                 170                 175
220 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
221             180                 185                 190
224 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
225             195                 200                 205
228 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
229     210             215                 220
232 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
233 225                 230                 235                 240
236 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
237             245                 250                 255
240 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
241             260                 265                 270
244 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
245             275                 280                 285
248 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
249     290                 295                 300
252 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
253 305                 310                 315                 320
256 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
257             325                 330                 335
260 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
261             340                 345                 350
264 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
265     355                 360                 365
268 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
269     370                 375                 380
272 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
273 385                 390                 395                 400
276 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
277             405                 410                 415
280 Ala Gly Lys Ala Leu
281             420
284 <210> SEQ ID NO: 3
286 <211> LENGTH: 777
288 <212> TYPE: DNA
290 <213> ORGANISM: Isochrysis galbana
294 <220> FEATURE:
296 <221> NAME/KEY: CDS
298 <222> LOCATION: (1)..(777)
300 <223> OTHER INFORMATION: Delta-9 elongase
304 <400> SEQUENCE: 3
305 atg gcc ctc gca aac gac gcg gga gag cgc atc tgg gcg gct gtg acc      48
306 Met Ala Leu Ala Asn Asp Ala Gly Glu Arg Ile Trp Ala Ala Val Thr
307 1               5                   10                  15
309 gac ccg gaa atc ctc att ggc acc ttc tcg tac ttg cta ctc aaa ccg      96
310 Asp Pro Glu Ile Leu Ile Gly Thr Phe Ser Tyr Leu Leu Leu Lys Pro
311             20                  25                  30
```

```
314 ctg ctc cgc aat tcc ggg ctg gtg gat gag aag aag ggc gca tac agg     144
315 Leu Leu Arg Asn Ser Gly Leu Val Asp Glu Lys Lys Gly Ala Tyr Arg
316         35                  40                  45
318 acg tcc atg atc tgg tac aac gtt ctg ctg gcg ctc ttc tct gcg ctg     192
319 Thr Ser Met Ile Trp Tyr Asn Val Leu Leu Ala Leu Phe Ser Ala Leu
320         50                  55                  60
322 agc ttc tac gtg acg gcg acc gcc ctc ggc tgg gac tat ggt acg ggc     240
323 Ser Phe Tyr Val Thr Ala Thr Ala Leu Gly Trp Asp Tyr Gly Thr Gly
324 65                  70                  75                  80
326 gcg tgg ctg cgc agg caa acc ggc gac aca ccg cag ccg ctc ttc cag     288
327 Ala Trp Leu Arg Arg Gln Thr Gly Asp Thr Pro Gln Pro Leu Phe Gln
328                     85                  90                  95
330 tgc ccg tcc ccg gtt tgg gac tcg aag ctc ttc aca tgg acc gcc aag     336
331 Cys Pro Ser Pro Val Trp Asp Ser Lys Leu Phe Thr Trp Thr Ala Lys
332                 100                 105                 110
334 gca ttc tat tac tcc aag tac gtg gag tac ctc gac acg gcc tgg ctg     384
335 Ala Phe Tyr Tyr Ser Lys Tyr Val Glu Tyr Leu Asp Thr Ala Trp Leu
336             115                 120                 125
338 agg gtc tcc ttt ctc cag gcc ttc cac cac ttt ggc gcg ccg tgg gat     432
339 Arg Val Ser Phe Leu Gln Ala Phe His His Phe Gly Ala Pro Trp Asp
340         130                 135                 140
342 gtg tac ctc ggc att cgg ctg cac aac gag ggc gta tgg atc ttc atg     480
343 Val Tyr Leu Gly Ile Arg Leu His Asn Glu Gly Val Trp Ile Phe Met
344 145                 150                 155                 160
347 ttt ttc aac tcg ttc att cac acc atc atg tac acc tac tac ggc ctc     528
348 Phe Phe Asn Ser Phe Ile His Thr Ile Met Tyr Thr Tyr Tyr Gly Leu
349                 165                 170                 175
351 acc gcc gcc ggg tat aag ttc aag gcc aag ccg ctc atc acc gcg atg     576
352 Thr Ala Ala Gly Tyr Lys Phe Lys Ala Lys Pro Leu Ile Thr Ala Met
353             180                 185                 190
355 cag atc tgc cag ttc gtg ggc ggc ttc ctg ttg gtc tgg gac tac atc     624
356 Gln Ile Cys Gln Phe Val Gly Gly Phe Leu Leu Val Trp Asp Tyr Ile
357             195                 200                 205
359 aac gtc ccc tgc ttc aac tcg gac aaa ggg aag ttg ttc agc tgg gct     672
360 Asn Val Pro Cys Phe Asn Ser Asp Lys Gly Lys Leu Phe Ser Trp Ala
361         210                 215                 220
363 ttc aac tat gca tac gtc ggc tcg gtc ttc ttg ctc ttc tgc cac ttt     720
364 Phe Asn Tyr Ala Tyr Val Gly Ser Val Phe Leu Leu Phe Cys His Phe
365 225                 230                 235                 240
367 ttc tac cag gac aac ttg gca acg aag aaa tcg gcc aag gcg ggc aag     768
368 Phe Tyr Gln Asp Asn Leu Ala Thr Lys Lys Ser Ala Lys Ala Gly Lys
369                 245                 250                 255
371 cag ctc tag                                                         777
372 Gln Leu
376 <210> SEQ ID NO: 4
378 <211> LENGTH: 258
380 <212> TYPE: PRT
382 <213> ORGANISM: Isochrysis galbana
386 <400> SEQUENCE: 4
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```
<210> SEQ ID NO 115
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Consensus
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(13)
<223> OTHER INFORMATION: Xaa in the sequence at positions 2, 3, 4, 6, 7, 8 and 9
has the
     meaning given in Table A.
<400> SEQUENCE: 115
     Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa
     1                                    10
```

Invalid Response: <213 Responses Can be either Artificial, Unknown or Genus Species. See Item 10 on Error Summary sheet.

Insufficient Explanation. Pls Explain Xaa Specifically.

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 09/05/2006
PATENT APPLICATION: US/10/590,457   TIME: 15:11:49

Input Set : **E:\Sequence Listing-13987-00020-US.txt**
Output Set: **N:\CRF4\09052006\J590457.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:115; Xaa Pos. 2,3,4,6,7,10,13
Seq#:116; Xaa Pos. 3,4.5.6
Seq#:139; Xaa Pos. 3,4
Seq#:140; Xaa Pos. 2,3,5,6
Seq#:141; Xaa Pos. 3
Seq#:142; Xaa Pos. 5,6
Seq#:185; N Pos. 3,18
Seq#:186; N Pos. 3,9,12,15,21

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:121,122,123,124,125,126,127,128,129,130,143,144,145,146,147,148,149,150
Seq#:151,152,153,154,155,156,157,158,159,160,161,162,163,164,165,166,167,168
Seq#:169,170,171,172,173,174,175,176,177,178,179,180,181,182,185,186,187,188
Seq#:189,190,191,192,203,204,205,206,207,208,209,210,211,212,213,214,215,216
Seq#:217,218,219,220,221,222,223,224,225,226,227,228,229,230,231,232,233,234
Seq#:235,236,237,238,239,240,241,242,243,244,245,246,247,248,249,250,251,252
Seq#:253,254,255

VERIFICATION SUMMARY　　　　　　　　　DATE: 09/05/2006
PATENT APPLICATION:　US/10/590,457　　　TIME: 15:11:49

Input Set : **E:\Sequence Listing-13987-00020-US.txt**
Output Set: **N:\CRF4\09052006\J590457.raw**

```
L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:0
L:13254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:0
L:14471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0
L:14498 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0
L:14525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0
L:14552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:15228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185 after pos.:0
L:15246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:186 after pos.:0
```